

09/147443

Fig. 1a

LD1-40-VH sequence

9 18 27 36 45 54

5' CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC CTG

 Q V K L L E S G G V V Q P G R S L

63 72 81 90 99 108
 AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT GCC ATG CAC TGG

 R L S C I A S G F T L R N Y A M H W ← CDR1 →

117 126 135 144 153 162
 GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATA TGG TTT GAT

 V R Q A P G K G L E W V A G I W F D ← CDR2 →

171 180 189 198 207 216
 GGA AGT AAC AAA AAC TAT GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA

 G S N K N Y A D S V K G R F T I S R ← CDR2 →

225 234 243 252 261 270
 GAC AAT TCC AAG AAC ACG CTG TAT CTG CAA CTG AAC AGC CTG AGA GAC GAG GAC

 D N S K N T L Y L Q L N S L R D E D

279 288 297 306 315 324
 ACG GCT GTG TAT TAT TGT GCG AGA GAG CGA GCA GCA CGT GGT ATT TCT AGG TTC

 T A V Y Y C A R E R A A R G I S R F ← CDR3 →

333 342 351 360 369 3'
 TAT TAC TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC CCA

 Y Y Y M D V W G K G T T V T V S P ← CDR3 →

09/147443

Fig. 1b

LD1-40-VL sequence

5' GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGC GAC AGA GTC ACC

V M T Q S P S S L S A S V G D R V T

63 ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT TGG TAT CAG CAG

I T C R A S Q S I R S H L N W Y Q Q

← CDR1 →

117 AAA CCA GGG AAA GCC CCT AAG TTG CTG ATC TAT GGT GCG TCC ACT TTG CAA AGT

K P G K A P K L L I Y G A S T L Q S

← CDR2 →

171 GGC GTC CCA TCA AGG TTC AGT GGC AGT GGC TCT GGG GCA GTT TTC ACT CTC ACC

G V P S R F S G S G S G A V F T L T

225 ATC GCC AGT CTA CAA CCT GAA GAT TTT GCA ACT TAC TAC TGT CAA GAG AGT TAC

I A S L Q P E D F A T Y Y C Q E S Y

← CDR3 →

279 AGT AAT CCT CTA ATC ACC TTC GGC CAA GGG ACA CGA CTG GAG ACT AAA 3'

S N P L I T F G Q G T R L E T K

09/147443 3/34

Fig. 2a

LD1-52-VH sequence

09/147443

Fig. 2b

LD1-52-VL sequence

9 18 27 36 45 54

5' GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC

V M T Q S P S S L S A S V G D R V T

63 72 81 90 99 108

ATC ACT TGC CGG GCA AGT CAG AAC ATT ATC CGC TAT TTA AAT TGG TAT CAG CAG

I T C R A S Q N I I R Y L N W Y Q Q

117 126 135 144 153 162

AAG CCA GGG AAA GCC CCT AGG CTC CTG ATC TAT GGT GCG TCC ACT TTG CAA AGT

K P G K A P R L L I Y G A S T L Q S

171 180 189 198 207 216

GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC

G V P S R F S G S G T D F T L T

225 234 243 252 261 270

ATC AGT AGT CTG CAA CCT GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC

I S S L Q P E D F A T Y Y C Q Q S Y

279 288 297 306 315

CGT ACC CCT CCA TTC ACT TTC GGC CCT GGG ACC AAA GTG GAG ATC AAA 3'

R T P P F T F G P G T K V E I K

CDR3 →

09/147443

Fig. 3a

LD1-84-VH sequence

5' CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG TCC CTG
 9 18 27 36 45 54
 Q V K L L E S G G V V Q P G G S L

 AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT GGC ATG CAC TGG
 63 72 81 90 99 108
 R L S C E A S G F T L R S S G M H W

 ← CDR1 →
 GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG GCA CTT ATA TGG TTT GAT
 117 126 135 144 153 162
 V R Q A P G K G L E W V A L I W F D

 ← CDR2 →
 GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA
 171 180 189 198 207 216
 G S I R S Y A E S V K G R F T I S R

 ← CDR2 →
 GAC ACT TCC AAG AAC ACC CTA TAT CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC
 225 234 243 252 261 270
 D T S K N T L Y L Q M R S L S A D D

 ACG GCT GTG TAT TAC TGT GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC
 279 288 297 306 315 324
 T A V Y Y C A R D K A V R G I S R Y

 ← CDR3 →
 AAC TAT TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 3'
 333 342 351 360 369
 N Y Y M D V W G K G T T V T V S S

 ← CDR3 →

09/147443

Fig. 3b

LD1-84-VL sequence

5' GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGA GAC AGA GTC ACC
 V M T Q S P S S L S A S I G D R V T

ATC ACC TGC CGG GCA AGT CAG AGT ATC ATC AGG TAT TTG AAT TGG TAT CAG CAC
 I T C R A S Q S I I R Y L N W Y Q H

AAA CCA GGA AAA GCC CCT AAA CTC CTC ATC TTT GCT GCA TCG AAT TTG CAA ACT
 K P G K A P K L L I F A A S N L Q T

GGG GTC CCA TCC AGG TTC AGT GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC
 G V P S R F S G S G S G T D F T L T

ATC AGT GAC CTG CAG CCT GAG GAT TTC GCA ACT TAC TAC TGT CAA CAG AGT TAC
 I S D L Q P E D F A T Y Y C Q Q S Y

AGT AGG CCG TTC ACT TTT GGC CGG GGG ACC AGC CTG GAC ATC AAA 3'
 S R P F T F G R G T S L D I K

CDR1 ← → CDR2 ← → CDR3 ← →

9 18 27 36 45 54
 63 72 81 90 99 108
 117 126 135 144 153 162
 171 180 189 198 207 216
 225 234 243 252 261 270
 279 288 297 306 315

7/34

09/147443

Fig. 4a

LD1-110-VH sequence

9	18	27	36	45	54
CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC CTG					
Q V K L L E S G G V V Q P G R S L					
63	72	81	90	99	108
AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT GCC ATG CAC TGG					
R L S C I A S G F T L R N Y A M H W					
117	126	135	144	153	162
GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATA TGG TTT GAT					
V R Q A P G K G L E W V A G I W F D					
171	180	189	198	207	216
GGA AGC AAC AAA AAC TAT GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA					
G S N K N Y A D S V K G R F T I S R					
CDR2					
225	234	243	252	261	270
GAC AAC TCC AAG AAC ACT CTG TTT CTG CAC ATG AAC AGC CTG AGA GCC GAG GAC					
D N S K N T L F L H M N S L R A E D					
279	288	297	306	315	324
ACG GCT ACA TAT TAC TGT GCG AGA GAG AGG GCG ATT CGG GGA ATC AGT AGA TAC					
T A T Y Y C A R E R A I R G I S R Y					
CDR3					
333	342	351	360	369	
AAT TAC TAC ATG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 3'					
N Y Y M D V W G K G T T V T V S S					
CDR3					

09/147443

Fig. 4b

LD1-110-VL sequence

5'

	9	18	27	36	45	54	
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC							
V M T Q S P S S L S A S V G D R V T							
	63	72	81	90	99	108	
ATC ACT TGC CGG GCA AGT CAG AGC ATT CGA AGC TCT TTA AAT TGG TAT CAG CAG							
I T C R A S Q S I R S S L N W Y Q Q							
	117	126	135	144	153	162	
AAA CCA GGG AAA GCC CCT AAA GTC CTG ATC TAT GCT GCA TCC AGT TTG CAA AGT							
K P G K A P K V L I Y A A S S L Q S							
	171	180	189	198	207	216	
GGG GTC CCA TCC AGG TTC AGT GGC AGA GGA TCT GGG ACA GAT TTC ACT CTC ACC							
G V P S R F S G R G S G T D F T L T							
	225	234	243	252	261	270	
ATC AGC AGT CTG CAG CCT GAA GAT TTT GCG ACT TAT TAT TGT CAA CAG AGT TCC							
I S S L Q P E D F A T Y Y C Q Q S S							
	279	288	297	306	315		
AGT TCC TCG TGG ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 3'							
S S S W T F G Q G T K V E I K							
<hr/> CDR3 →							

09/147443

Fig. 5a

LD1-117-VH sequence

5' CAG GTG AAA CTG CTC GAG TCA GGA GGC GTG GTC CAG CCT GGG AAG TCC CTG
 Q V K L L E S G G V V Q P G K S L

9 18 27 36 45 54

 R L S C A A S G F S F N S H G M H W
 63 72 81 90 99 108

AGA CTT TCC TGT GCA GCG TCT GGA TTC AGT TTC AAT AGC CAT GGC ATG CAC TGG

 117 126 135 144 153 162

GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA TTT ATA TGG TTT GAT
 V R Q A P G K G L E W V A F I W F D

 171 180 189 198 207 216

GGC AGT AAT AAA TAC TAT GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC ACC AGA
 G S N K Y Y A D S V K G R F T I T R

 225 234 243 252 261 270

GAC AAC TCC AAG AAC ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC
 D N S K N T L Y L Q M N S L R A E D

 279 288 297 306 315 324

ACG GCT GTC TAT TAC TGT GCG AGA GAG ACC TCA GTA AGG CTA GGG TAT AGC CGC
 T A V Y Y C A R E T S V R L G Y S R

 333 342 351 360 369 378

TAC AAT TAC TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC ATC TCG TCA 3'
 Y N Y Y M D V W G K G T T V T I S S

 CDR3 →

09/147443

Fig. 5b

LD1-117-VL sequence

5'

	9	18	27	36	45	54	
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC							
V M T Q S P S S L S A S V G D R V T							
	63	72	81	90	99	108	
ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT TGG TAT CAG CAG							
I T C R A S Q S I R S H L N W Y Q Q							
	← CDR1 →						
	117	126	135	144	153	162	
AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT GCA TCC AGT TTG CAA GGT							
K P G K A P K L L I Y A A S S L Q G							
	← CDR2 →						
	171	180	189	198	207	216	
GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC							
G V P S R F S G S G S G T D F T L T							
	225	234	243	252	261	270	
ATC AGC AGT CTG CAA CCT GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG AGT TAC							
I S S L Q P E D F A T Y Y C Q Q S Y							
	279	288	297	306	315		
AGG GCC CCT CAG TGG ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 3'							
R A P Q W T F G Q G T K V E I K							
← CDR3 →							

11/34

09/147443

Fig. 6a

LD2-1-VH sequence

5' CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG TCC CTG 54

Q V K L L E S G G V V Q P G G S L

63 72 81 90 99 108

AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT GGC ATG CAC TGG

R L S C V A S G F T L R S Y G M H W

117 126 135 144 153 162

GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG GCT TTT ATA TGG TTT GAT

V R Q A P G K G L E W V A F I W F D

171 180 189 198 207 216

GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC CGA

G S N K G Y V D S V K G R F T I S R

CDR2 →

225 234 243 252 261 270

GAC AAT TCC AAG AAC ATG GTC TAT CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC

D N S K N M V Y L Q M N S L R A D D

279 288 297 306 315 324

ACG GCT GTA TAT TAT TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC

T A V Y Y C A R E K A L R G I S R Y

CDR3 ←

333 342 351 360 369

AAC TAT TAC CTG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 3'

N Y Y L D V W G K G T T V T V S S

CDR3 →

12/34

09/147443

Fig. 6b

LD2-1-VL sequence

5' GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGA CAG AGG GTC ACC ATC
 V V T Q P P S A S G T P G Q R V T I

TCT TGT TCT GGA AGC AAC TCC ATC CTT GGA AGT AAG TAT GTA TAC TGG TAC CAG
 S C S G S N S I L G S K Y V Y W Y Q

AAA CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT AAG AAT GAT CAG CGG CCC
 K L P G T A P K L L I Y K N D Q R P

TCA GGG GTC TCT GAC CGA TTC TCT GGC TCC AAG TCT GGC ACC TCG GCC TCC CTG
 S G V S D R F S G S K S G T S A S L

GCC ATC AGT GGG CTC CGG TCC GAG GAT GAG GCT GAC TAT TAC TGT GCA CCA TGG
 A I S G L R S E D E A D Y Y C A P W

GAT GCC AAC CTG GGT GGC CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA
 D A N L G G P V F G G G T K L T V L

AGT CAG CCC 3'
 S Q P

9 18 27 36 45 54
 63 72 81 90 99 108
 117 126 135 144 153 162
 171 180 189 198 207 216
 225 234 243 252 261 270
 279 288 297 306 315 324
 333

09/147443

Fig. 7a

LD2-4-VH sequence

5' CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG TCC CTG
 9 18 27 36 45 54
 Q V K L L E S G G V V Q P G G S L

 AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT GGC ATG CAC TGG
 63 72 81 90 99 108
 R L S C E A S G F T L R S S G M H W

 GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG GCA CTT ATA TGG TTT GAT
 117 126 135 144 153 162
 V R Q A P G K G L E W V A L I W F D

 GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA
 171 180 189 198 207 216
 G S I R S Y A E S V K G R F T I S R

 CDR2 →
 GAC ACT TCC AAG AAC ACC CTA TAT CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC
 225 234 243 252 261 270
 D T S K N T L Y L Q M R S L S A D D

 ACG GCT GTG TAT TAC TGT GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC
 279 288 297 306 315 324
 T A V Y Y C A R D K A V R G I S R Y

 CDR3 ←
 AAC TAT TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 3'
 333 342 351 360 369
 N Y Y M D V W G K G T T V T V S S

 CDR3 →

09/147443

Fig. 7b

LD2-4-VL sequence

5' GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC 54
 ----- V M T Q S P S S L S A S V G D R V T
 9 18 27 36 45 54
 ATC ACT TGC CGG ACA AGT CAG ACC ATT AGC AGA AAT TTA AAT TGG TAT CAG CAG 108
 ----- I T C R T S Q T I S R N L N W Y Q Q
 63 72 81 90 99 108
 AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT ACA TCC AGT TTG CAA AGT 162
 ----- K P G K A P K L L I Y A T S S L Q S
 117 126 135 144 153 162
 GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC 216
 ----- G V P S R F S G S G S G T D F T L T
 171 180 189 198 207 216
 ATC AAT AGT CTA CAA CCT GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC 270
 ----- I N S L Q P E D F A T Y Y C Q Q S Y
 225 234 243 252 261 270
 ACT ACC CCT TCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 315 3'
 ----- T T P S F G Q G T K V E I K
 CDR3 →

09/147443

Fig. 8a

LD2-5-VH sequence

LD2-5-VH sequence

5'	CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCG GGG GGG TCC CTG	9 18 27 36 45 54
	Q V K L L E S G G L V Q P G G S L	
	AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AGT TAT GGC ATG CAC TGG	63 72 81 90 99 108
	R L S C V A S G F T F R S Y G M H W	
	GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG GCT TTT ATA TGG TTT GAT	117 126 135 144 153 162
	V R Q A P G K G L E W V A F I W F D	
	GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC CGA	171 180 189 198 207 216
	G S N K G Y V D S V K G R F T I S R	
	GAC AAT TCC AAG AAC ATG CTC TAT CTG CAA ATG AAT AGC CTG AGA GCC GAG GAC	225 234 243 252 261 270
	D N S K N M L Y L Q M N S L R A E D	
	ACG GCT GTA TAT TAT TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC	279 288 297 306 315 324
	T A V Y Y C A R E K A L R G I S R Y	
	AAC TAT TAC CTG GAC GTC TGG GGC AAG GGG GCC ACG GTC ACC GTC TCC TCA 3'	333 342 351 360 369
	N Y Y L D V W G K G A T V T V S S	
CDR3		

09/147443

Fig. 8b

LD2-5-VL sequence

5' GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGC GAC AGA GTC ACC

V M T Q S P S S L S A S I G D R V T

ATC ACT TGC CGG GCA AGT CAG AGC GTT ACC AGG TCT TTA AAT TGG TAT CAG CAG

I T C R A S Q S V T R S L N W Y Q Q

AAA CCA GGG AAA GCC CCT AGG CTC CTA ATC TTT GCT GCG TCC ACT TTG CAA AGT

K P G K A P R L L I F A A S T L Q S

CDR1 ← → 117 126 135 144 153 162

GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA TCT GGG ACA GAT TTC ACC CTC ACC

G V P S R F S G S G S G T D F T L T

225 234 243 252 261 270

ATC AGC AGT CTG CAA CCT GAG GAT TTT GGA ACT TAC TAC TGT CAA CAG AAT TAC

I S S L Q P E D F G T Y Y C Q Q N Y

CDR2 ← → 171 180 189 198 207 216

AGG ACC CCT CAG TGG ACG TTC GGC CAA GGG ACC AAG GTA GAA ATC AAA 3'

R T P Q W T F G Q G T K V E I K

CDR3 ← → 279 288 297 306 315

09/147443

Fig. 9a

LD2-10-VH sequence

5' CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG TCC CTG 54

Q	V	K	L	L	E	S	G	G	V	V	Q	P	G	G	S	L
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

63 AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT GGC ATG CAC TGG 108

R	L	S	C	V	A	S	G	F	T	L	R	S	Y	G	M	H	W
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

117 GTC CGC CAG GCT CCA GGC AAG GGC 126 CTG 135 GAG TGG 144 GTG 153 162 GAT

V	R	Q	A	P	G	K	G	L	E	W	V	A	F	I	W	F	D
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

171 GGA AGT AAT AAA GGA TAT GTA GAC 180 TCC 189 GTG AAG 198 CGA 207 216 GAT

G	S	N	K	G	Y	V	D	S	V	K	G	R	F	T	I	S	R
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

225 GAC AAT TCC AAG AAC ATG GTC 234 TAT 243 CTG 252 CAA ATG AAC 261 270 AGC GAT

D	N	S	K	N	M	V	Y	L	Q	M	N	S	L	R	A	D	D
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

279 ACG GCT GTA TAT TAT 288 TAT TGT GCG 297 AGA GAG AAG 306 GCG 315 324 GAG

T	A	V	Y	Y	Y	C	A	R	E	K	A	L	R	G	I	S	R
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

333 TAC AAC TAT TAC CTG 342 GAC GTC TGG 351 GGC AAG GGG 360 ACC ACG 369 378 GTC ACC GTC TCC TCA

Y	N	Y	Y	L	D	V	W	G	K	G	T	T	V	T	V	S	S
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

3' CDR3 ----->

09/147443

Fig. 9b

LD2-10-VL sequence

5' GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG TCC CCA GGA GGG ACA GTC ACT CTC
 V V T Q E P S L T V S P G G T V T L

ACC TGT GCT TCC AGC ACT GGG GCA GTC ACC AGG GGT TAC TAT CCA AAC TGG TTC
 T C A S S T G A V T R G Y Y P N W F

CAG CAG CCT GGA CAA GCA CCC AGG GCA CTG ATT TAT AGT ACA AAC AAA AAA
 Q Q K P G Q A P R A L I Y S T N K K

CAC TCC TGG ACC CCT GCC CGG TTC TCA GGC TCC CTC CTT GGG GGC AAA GCT GCC
 H S W T P A R F S G S L L G G K A A

CTG ACA CTG TCA GGT GTG CAG CCT GAA GAC GAG GCT GAA TAT TAC TGC CTG CTC
 L T L S G V Q P E D E A E Y Y C L L

TAC TAT GGT GGT GCT CAA CTC GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA
 Y Y G G A Q L V F G G G T K L T V L

CGT CAG CCC 3'
 R Q P

9 18 27 36 45 54
 63 72 81 90 99 108
 117 126 135 144 153 162
 171 180 189 198 207 216
 225 234 243 252 261 270
 279 288 297 306 315 324

CDR1 ← →
 CDR2 ← →
 CDR3 ← →

19/34

09/147443

Fig. 10a

LD2-11-VH sequence

5' CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG TCC CTG

 Q V K L L E S G G V V Q P G G S L

63 18 27 36 45 54
 AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT GGC ATG CAC TGG

 R L S C E A S G F T L R S S G M H W
 ← → CDR1
 117 126 135 144 153 162
 GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG GCA CTT ATA TGG TTT GAT

 V R Q A P G K G L E W V A L I W F D
 ← → CDR2
 171 180 189 198 207 216
 GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA

 G S I R S Y A E S V K G R F T I S R
 ← → CDR2
 225 234 243 252 261 270
 GAC ACT TCC AAG AAC ACC CTA TAT CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC

 D T S K N T L Y L Q M R S L S A D D
 279 288 297 306 315 324
 ACG GCT GTG TAT TAC TGT GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC

 T A V Y Y C A R D K A V R G I S R Y
 ← → CDR3
 333 342 351 360 369
 AAC TAT TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 3'

 N Y Y M D V W G K G T T V T V S S
 ← → CDR3

09/147443

Fig. 10b

LD2-11-VL sequence

5' GTG TTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA CGA GAC AGA GTC ACC
 V L T Q S P S S L S A S I R D R V T

ATC ACT TGC CGG GCA AGT CAG AAC ATT GGC AGT TAT TTA AAT TGG TAT CAG CAC
 I T C R A S Q N I G S Y L N W Y Q H

AAA CCA GGG ACA GCC CCT AAA CTC CTG ATC TAT GCT GTA TCC GCT TTG CAA AGT
 K P G T A P K L L I Y A V S A L Q S

GGG GTC CCA TCG AGG TTC AGT GGC AGT AGA TCT GGG ACA GAT TTC ACT CTC ACC
 G V P S R F S G S R S G T D F T L T

ATC AGC AGT CTG CAA CCT GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC
 I S S L Q P E D F A T Y Y C Q Q S Y

AGT CCC CCG TAC ACT TTC GGC CAG GGG ACC AAC CTG CAG ATC AAA 3'
 S P P Y T F G Q G T N L Q I K

CDR1 ← →
 CDR2 ← →
 CDR3 ← →

09/147443

Fig. 11a

LD2-14-VH sequence

5' CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG TCC CTG ---
 Q V K L L E S G G V V Q P G G S L

 9 18 27 36 45 54
 AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT GGC ATG CAC TGG
 R V A C V A S G F T F R N F G M H W

 63 72 81 90 99 108
 GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCT TTT ATT TGG TTT GAT
 V R Q A P G K G L E W V A F I W F D

 117 126 135 144 153 162
 GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT AAG GGC CGA TTC ACC GTC TCC AGA
 A S N K G Y G D S V K G R F T V S R

 171 180 189 198 207 216
 GAC AAT TCC AAG AAC ACG CTC TAT CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC
 D N S K N T L Y L Q M N G L R A E D

 225 234 243 252 261 270
 ACG GCT GTA TAT TAT TGT GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC
 T A V Y Y C A R E K A V R G I S R Y

 279 288 297 306 315 324
 AAC TAC TAC ATG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 3'
 N Y Y M D V W G K G T T V T V S S

 333 342 351 360 369
 CDR3 → CDR3 → CDR3 → CDR3 →

09/147443

Fig. 11b

LD2-14-VL sequence

5' GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA GAC AGA GTC ACC 54
 V M T Q S P S S L S A S V G D R V T

ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AAC AAT TTA AAT TGG TAT CAG CAG 108
 I T C R A S Q S I I N N L N W Y Q Q

AAA CCA GGC AAA GCC CCT GAA CTC CTG ATC TAT GCT GCA TCC AGT TTG CAA AGT 117 126 135 144 153 162
 K P G K A P E L L I Y A A S S L Q S

GGG GTC CCT TCA AGG TTC CGT GGC AGT GGA TCT GGG AGA GAT TTC ACT CTC ACC 171 180 189 198 207 216
 G V P S R F R G S G S G R D F T L T

GTC ACC AGT CTG CAA CCT GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC 225 234 243 252 261 270
 V T S L Q P E D F A T Y Y C Q Q S Y

AGT ACC CTG TGG ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 3' 279 288 297 306 315
 S T L W T F G Q G T K V E I K

CDR1 ← → 117 126 135 144 153 162
 CDR2 ← → 171 180 189 198 207 216
 CDR3 ← → 279 288 297 306 315

23/34
09/147443

Fig. 12a

LD2-17-VH sequence

5'	CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG TCC CTG	9 18 27 36 45 54
	Q V K L L E S G G V V Q P G G S L	

	AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AGT TAT GGC ATG CAC TGG	63 72 81 90 99 108
	R L S C V A S G F T F R S Y G M H W	

	GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG GCT TTT ATA TGG TTT GAT	117 126 135 144 153 162
	V R Q A P G K G L E W V A F I W F D	

	GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC CGA	171 180 189 198 207 216
	G S N K G Y V D S V K G R F T I S R	

	GAC AAT TCC AAG AAC ACG CTC TAT CTG CAA ATG AAG AGC CTG AGA GCC GAG GAC	225 234 243 252 261 270
	D N S K N T L Y L Q M K S L R A E D	

	ACG GCT GTA TAT TAT TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC	279 288 297 306 315 324
	T A V Y Y C A R E K A L R G I S R Y	

	AAC TAT TAC CTG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA	333 342 351 360 369 3'
	N Y Y L D V W G K G T T V T V S S	

	CDR3 →	

Fig. 12b

LD2-17-VL sequence

5' GTG ATG ACC CAG TCT CCA TTC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC
 V M T Q S P F S L S A S V G D R V T

ATC ACT TGC CGG GCA AGT CAG AAC ATT AGG AGT TTT TTA AGT TGG TAT CAG CAG
 I T C R A S Q N I R S F L S W Y Q Q

AAA CCA GGG ACA GCC CCT AAG CTC CTG ATC TAT GCT GCA TCC AGG TTG CAA AGT
 K P G T A P K L L I Y A A S R L Q S

GGG GTC CCA TCA AGG TTC AGT GGC AGT GGG TCT GGG ACA GAT TTC ACT CTC ACC
 G V P S R F S G S G T D F T L T

ATC AGC ACT CTG CAA CCT GAA GAT TTT GCG ACT TAC TAC TGT CAA CAG AGT TAC
 I S T L Q P E D F A T Y Y C Q Q S Y

AGT GCC CCT TGG ACG TTC GGC CAA GGG ACC AAG CTG GAA ATC AAA 3'
 S A P W T F G Q G T K L E I K

CDR1 ← → 117 126 135 144 153 162
 CDR2 ← → 171 180 189 198 207 216
 CDR3 ← → 225 234 243 252 261 270

25/34
09/147443

Fig. 13a

LD2-20-VH sequence

5'	CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG TCC CTG	9 18 27 36 45 54
	Q V K L L E S G G V V Q P G G G S L	

	AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TCC AGG AGT TAT GGC ATG CAC TGG	63 72 81 90 99 108
	R L S C V A S G F T S R S Y G M H W	

	GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG GCT TTT ATA TGG TTT GAT	117 126 135 144 153 162
	V R Q A P G K G L E W V A F I W F D	

	GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC CGA	171 180 189 198 207 216
	G S N K G Y V D S V K G R F T I S R	

	GAC AAT TCC AAG AAC ACG CTC TAT CTG CAA ATG AAG AGC CTG AGA GCC GAG GAC	225 234 243 252 261 270
	D N S K N T L Y L Q M K S L R A E D	

	ACG GCT GTA TAT TAT TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC	279 288 297 306 315 324
	T A V Y Y C A R E K A L R G I S R Y	

	AAC TAT TAC CTG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA	333 342 351 360 369 3'
	N Y Y L D V W G K G T T V T V S S	

3'	CDR3	CDR3

09/147443

Fig. 13b

LD2-20-VL sequence

5' GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC
 V M T Q S P S S L S A S V G D R V T
 ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AGC TAT TTA AAT TGG TAT CAG CAG
 I T C R A S Q S I S S Y L N W Y Q Q
 ← CDR1 →
 AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT GCA TCC AGT TTG CAA AGT
 K P G K A P K L L I Y A A S S L Q S
 ← CDR2 →
 GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC
 G V P S R F S G S G T D F T L T
 ATC AGC AGT CTG CAA CCT GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC
 I S S L Q P E D F A T Y Y C Q Q S Y
 ← CDR3 →
 AGT ACC CGA TTC ACT TTC GGC CCT GGG ACC AAA GTG GAT ATC AAA 3'
 S T R F T F G P G T K V D I K

27/34

09/147443

Fig. 14a

LD1-6-17-VH sequence

5' CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC CTG 54
 Q V K L L E S G G V V Q P G R S L

 63 72 81 90 99 108
 AGA CTT TCC TGT GCA GCG TCT GGA TTT ACC TTC AGT AGC TAT GGC ATG CAC TGG
 R L S C A A S G F T F S S Y G M H W

117 126 135 144 153 162
 GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GAT ATA TGG TTT GAT
 V R Q A P G K G L E W V A D I W F D

171 180 189 198 207 216
 GGA GGT AAT AAA CAT TAT GCA GAC TTC GTG AAG GGC CGA TTC ACC ATC TCC AGA
 G G N K H Y A D F V K G R F T I S R

225 234 243 252 261 270
 GAC AAT TCC AAG AAC ACG GTG TAT CTA CAA ATG AAC AGC CTG AGA GTC GAG GAC
 D N S K N T V Y L Q M N S L R V E D

279 288 297 306 315 324
 ACG GCT GTG TAT TAC TGT GCG AGG GAT TAC TAT AGC GTT ACT AAG AAA CTC AGA
 T A V Y Y C A R D Y Y S V T K K L R

333 342 351 360 369 378
 CTC CAC TAC TAC TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC
 L H Y Y Y M D V W G K G T T V T V

TCC TCA 3'
 S S

09/147443

Fig. 14b

LD1-6-17-VL sequence

5' GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC 54
 V M T Q S P S S L S A S V G D R V T

ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA ACC TGG TAT CAG CAA 108
 I T C R A S Q G I R N D L T W Y Q Q

AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT GCA TCC AAT TTA CAA AGT 162
 K P G K A P K L L I Y A A S N L Q S

GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGC ACA GAT TTC ACT CTC ACC 216
 G V P S R F S G S G S G T D F T L T

ATC AGC AGC CTG CAG CCT GAA GAT TTT GCA ACT TAT TAC TGT CTA CAA GAT AAC 270
 I S S L Q P E D F A T Y Y C L Q D N

AAT TTC CCG TAC ACT TTT GGC CAG GGG ACC AAG CTG GAG ATC AAA 3' 315
 N F P Y T F G Q G T K L E I K

CDR1 ← → CDR2 ← → CDR3 ← →

09/147443

Fig. 15a

LD1/2-6-3-VH sequence

09/147443

Fig. 15b

LD1/2-6-3-VL sequence

9 18 27 36 45 54

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC

V M T Q S P S S L S A S V G D R V T

63 72 81 90 99 108

ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT TGG TAT CAG CAC

I T C R A S Q S I I R Y L N W Y Q H

← CDR1 →

117 126 135 144 153 162

AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT ACT GCA TCC AGT TTG CAA AGT

K P G K A P K L L I H T A S S L Q S

← CDR2 →

171 180 189 198 207 216

GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA TCT GGG ACA GAT TTC ACT CTC ACC

G V P S R F S G S V S G T D F T L T

225 234 243 252 261 270

ATC AGC AGT CTG CAA CCT GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC

I S S L Q P E D F A T Y Y C Q Q S Y

← CDR3 →

279 288 297 306 315 3'

ACT ACC CCG TAC ACT TTT GGC CAG GGG ACC AAG CTG CAG ATC AAA

T T P Y T F G Q G T K L Q I K

09/147443

Fig. 16a

LD1/2-6-33-VH sequence

5' CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG TCC CTG
 9 V K L L E S G G V V Q P G G S L

 AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT GGC ATG CAC TGG
 63 R V A C V A S G F T F R N F G M H W

 GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCT TTT ATT TGG TTT GAT
 117 V R Q A P G K G L E W V A F I W F D

 GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT AAG GGC CGA TTC ACC GTC TCC AGA
 171 A S N K G Y G D S V K G R F T V S R

 CDR2 →
 GAC AAT TCC AAG AAC ACG CTC TAT CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC
 225 D N S K N T L Y L Q M N G L R A E D

 ACG GCT GTA TAT TAT TGT GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC
 279 T A V Y Y C A R E K A V R G I S R Y

 CDR3 ←
 AAC TAC TAC ATG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 3'
 333 N Y Y M D V W G K G T T V T V S S

 CDR3 →

09/147443

Fig. 16b

LD1/2-6-33-VL sequence

5' GTG ATG ACC CAG TCT CCA TCC TTC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC 54
 V M T Q S P S F L S A S V G D R V T

ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT TGG TAT CAG CAC 108
 I T C R A S Q S I I R Y L N W Y Q H

AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT GCT GCA TCC AGT TTG CAA AGT 162
 K P G K A P K L L I H A A S S L Q S

GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA TCT GGG ACA GAT TTC ACT CTC ACC 216
 G V P S R F S G S V S G T D F T L T

ATC AGC AGT CTG CAA CCT GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC 270
 I S S L Q P E D F A T Y Y C Q Q S Y

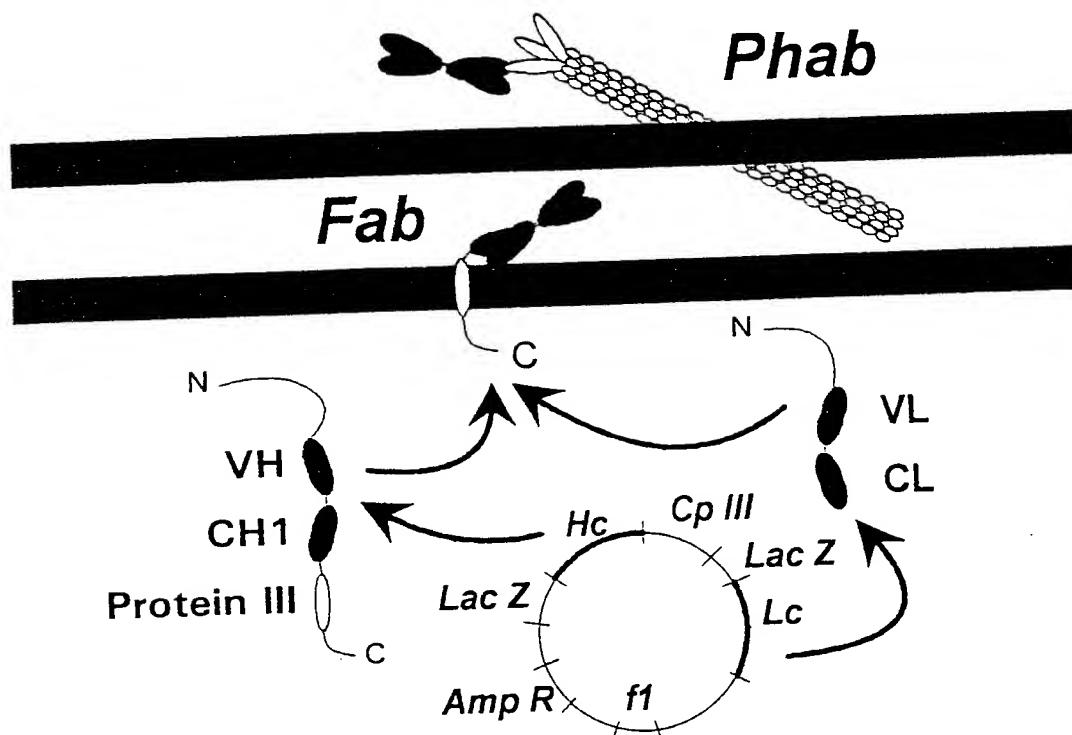
ACT ACC CCG TAC ACT TTT GGC CAG GGG ACC AAG CTG CAG ATC AAA 3'
 T T P Y T F G Q G T K L Q I K

CDR1 ← →
 CDR2 ← →
 CDR3 ← →

09/147443

Fig. 17

The pComb3 Expression System



09/147443

34/34

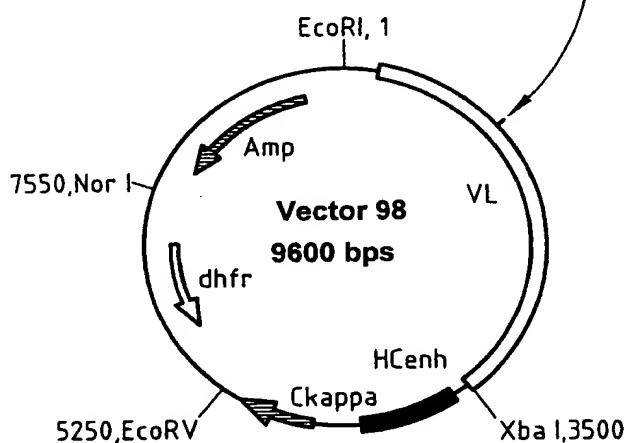
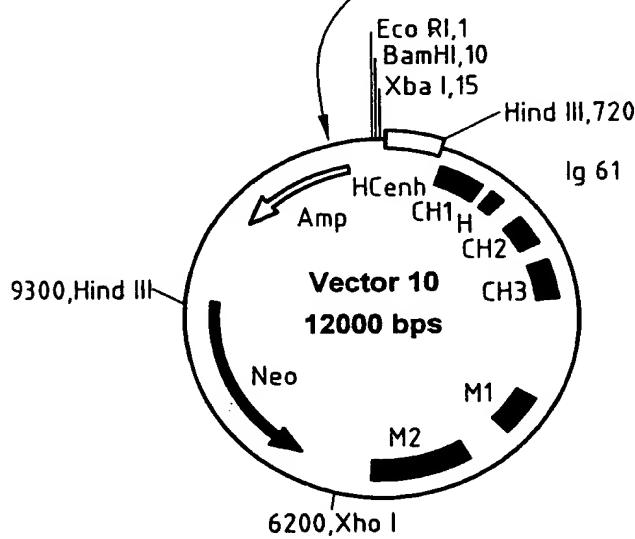
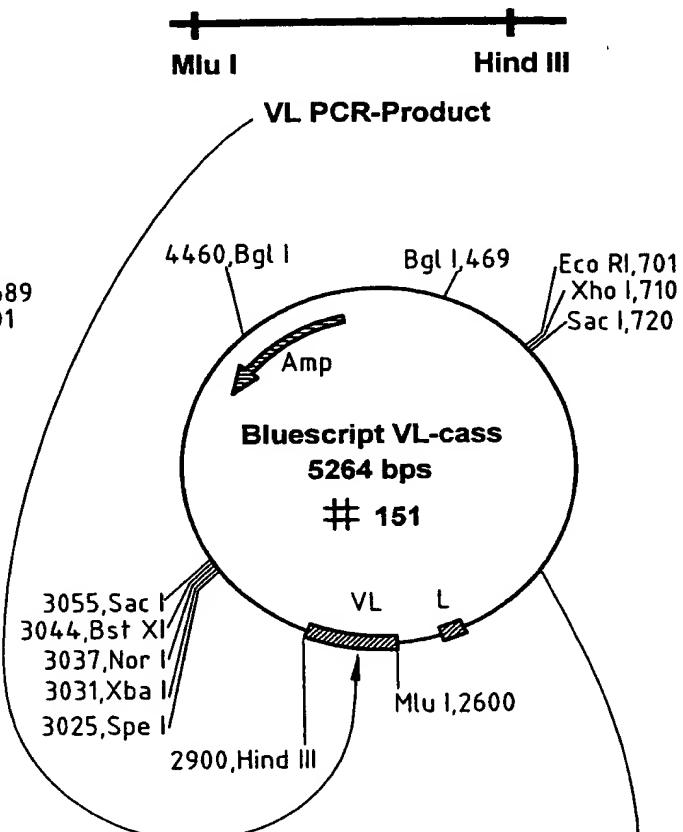
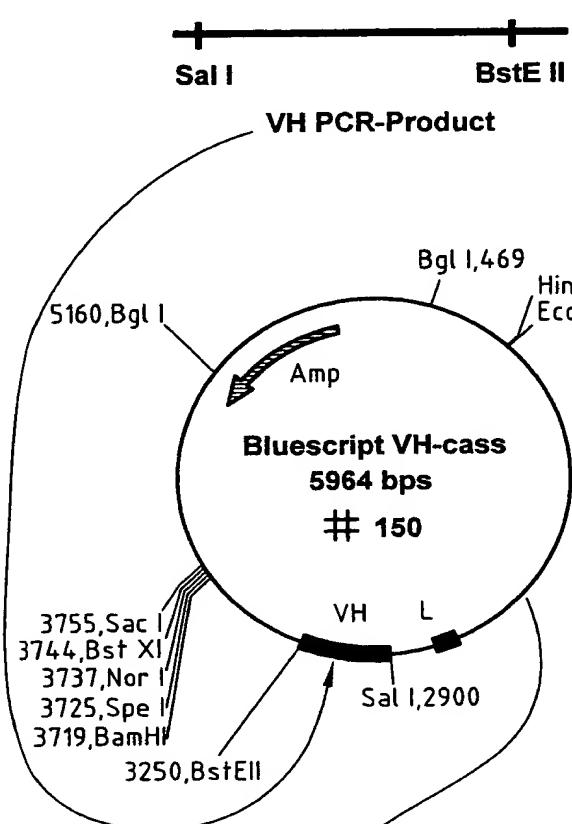


FIG. 18

FIG. 19